Antiproliferative, Antioxidant and Binding Mechanism Analysis of Prodigiosin from Newly Isolated Radio-resistant Streptomyces sp. Strain WMA-LM31

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Background: The objective of this study was to isolate a radio-resistant strain and screen their potential colored compounds for antioxidative and anticancerous activitie. Moreover a molecular docking approach was adopted to understand theoretical binding mechanism and affinity of prodigiosin for anti-cancer targets and protein damage inhibition.

Methods and Results: A radio-resistant bacterium, labelled as strain WMA-LM31, was isolated from desert soil. 16S rRNA gene sequencing showed that the bacterium clusters to genus Streptomyces. Streptomyces sp. strain WMA-LM31 was found resistant to the maximum ultraviolet radiation dosage of 2×103 J/m2. Strain WMA-LM31 produced a red color pigment in tryptone glucose yeast (TGY) medium. The pigment was extracted in methanol and purified by column chromatography. LCMS analysis of the compound showed its molar mass 324 [m/z]+ and chemical formula C20H25N3O, hence identified as prodigiosin. The purified prodigiosin showed strong antioxidant (62.51%) activities. Moreover, a high inhibitory action against oxidative damages to bovine serum albumin and mice liver lipids was studied. IC50 values of HepG2 and HeLa cell lines was found at 12.66 and 14.83 μg/ml of prodigiosin concentration, respectively. Furthermore, molecular docking with two different cancer macromolecular targets: (2O2F (Bcl-2) and 1DI8 (CDK-2), and bovine serum albumin (PDB id: 3V03) showed that binding pattern analysis indicated the affinity of compound is due to the presence of terminal pyrrole rings.

Conclusions: It is concluded, that prodigiosin pigment extracted from Streptomyces WMA-LM31 has strong anticancer, apoptotic and antioxidant properties. The role of centeral pyrrole ring was investigated to interact through strong bonding and vander waal forces with protein residues: Phe76, His78, Gln79, Asp80 and Lys83 that contribute to its anticancerous and protein preventing abilities.

The knowledge of binding mechanisms and interactions of prodigiosin isolated from (bacteria) could provide future directions in designing potent leads to cancer targets.

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Public health hazard due to antibiotic resistant Staphylococcus aureus

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Staphylococcus aureus (S.aureus) is a pathogenic bacterium that is consider as a threat to both animals and human. S. aureus is perhaps a most successful pathogen of genus Staphyloccoci because of its ability to cause a wide range of life threatening infections, its intrinsic virulence and its capability to adapt to different environmental conditions. The emergence and dissemination of antibiotic resistant strains of S.aureus is a great challenge for medical sector. Antibiotic resistance in S.aureus leads to increase in the cost of treatment and difficulty in the treatment of its infections. The present study was conducted to determine the frequency of S.aureus recovered from different clinical samples and their antibiotic susceptibility profiles. Molecular investigation was done by targeting the genetic determinants involved in antibiotic resistance. For molecular identifications the blaZ and mecA gene were amplified. Statistical and bioinformatics analysis was done to find out the resistance frequency and molecular characterization. The results of present study revealed the high rate of resistance against; methacilline and beta lactam antibiotics in S.aureus. These two are commonly used antibiotics and these findings have prompting concern with rational use of antibiotics.

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Laboratory Based Surveillance of Pneumococcal Serotypes causing Invasive and Non-Invasive Infections in Karachi, Pakistan

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a. Background: Streptococcus pneumonia is a common pathogen associated with invasive and non-invasive infections. In Pakistan annually 600,000 cases of pneumococcal infections are reported. Knowledge of pneumococcal serotypes in a population is important for guiding vaccine formulation. This is the first study from Pakistan describing pneumococcal serotypes causing invasive and non-invasive infections in Pakistan.

b. Objective: To determine the serotype distribution of pneumococcal isolates causing invasive and non-invasive disease in Karachi, Pakistan.

c. Methods: This was a cross sectional study conducted at PMRC Research Centre, JPMC in collaboration with Aga Khan University Hospital Karachi, Liaquat National Hospital Karachi and Ziauddin Hospital Karachi. Clinical isolates of S. pneumoniae from three major microbiology laboratories of Karachi were collected and tested for sensitivity patterns against commonly used antibiotics and serotype. Serotyping was done through sequential multiplex PCR method as described by CDC-USA to determine the distribution of different pneumococcal serotypes in our population.

d. Results: Total 245 pneumococcal isolates were collected from collaborating laboratories including 155 (63.6%) from hospitalized and 88(35.9%) from non-hospitalized patients. Invasive infections were significantly higher (70.7%) in children <5 years while elderly had a high proportion (54.5%) of non-invasive infections (p-value 0.006). Serogroup 6A/6B/6C/6D (9.2%) was the most commonly isolated serogroup followed by serotype 1(7.9%), 19A (5.8%), 3 (5.8%), 19F (5.4%) while 46 (19.2%) isolates were not type-able by multiplex PCR.

e. Conclusions: Serogroups 6A/6B/6C/6D is most commonly involved in infections among our population followed by serotype 1 and 19A hence vaccines targeting these serotypes may be effective in our population. Continuous surveillance of pneumococcal infections and serotypes is important to evaluate the impact of vaccine introduction.

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